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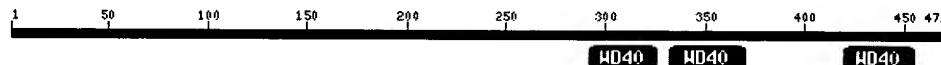
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Query= gi|10177650|dbj|BAB11112.1| cell cycle switch protein
[Arabidopsis thaliana]
(472 letters)

Database: oasis_sap.v1.58

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Query: gi|10177650 (NM_121387) fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
 Matching gi: [15240729](#)

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178 BLAST hits to 29 unique species [Sort by taxonomy proximity](#)

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472 aa					
	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
---	2462	19	AAM20433	20466231	cell cycle switch protein [Arabidopsi
---	1445	19	CAA19806	3292816	putative fizzy-related protein [Arabidop
---	1445	19	AAM20437	20466239	putative fizzy-related protein [Arabidop
---	1436	19	AAL36231	17380838	putative Srwl protein [Arabidopsis thal
---	1434	14	AAD22612	4558462	cell cycle switch protein [Medicago sativa
---	1434	14	AAF37386	7158292	WD-repeat cell cycle regulatory protein [Arabidopsis thaliana]
---	1415	19	CAB44330	5002527	Srwl-like protein [Arabidopsis thaliana]
---	1407	11	BAB63690	15289995	putative cell cycle switch protein [Arabidopsis thaliana]
---	1399	19	NP_194022	22328875	fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
---	1192	3	CAA74576	2326943	fizzy-related protein [Xenopus laevis]
---	1183	3	AAC62835	3702286	R33374_1 [Homo sapiens]
---	1183	3	BAA86556	6330805	KIAA1242 protein [Homo sapiens]
---	1181	3	BAA86954	6463679	Fzr1 [Homo sapiens]
---	1181	3	AAD52029	5813825	fizzy-related protein [Mus musculus]
---	1167	3	AAF20266	6642733	fizzy-related protein homolog [Homo sapiens]
---	1164	3	AAF45973	7290520	fzr gene product [Drosophila melanogaster]
---	1164	3	CAA74575	2326419	fizzy-related protein [Drosophila melanogaster]
---	1134	3	EAA00976	21288683	agCP12792 [Anopheles gambiae str. PEST]
---	1080	3	AAL31949	16930527	CDH1-C [Gallus gallus]
---	1060	3	CAA87433	3881613	contains similarity to Pfam domain: CDH1
---	1034	3	AAL31947	16930523	CDH1-A [Gallus gallus]
---	999	3	BAA22152	2381494	Srwl [Schizosaccharomyces pombe]
---	983	3	CAA22522	4049501	WD domain; G beta repeat protein [Schizosaccharomyces pombe]
---	922	3	AAF47111	7291689	CG16783-PA [Drosophila melanogaster]
---	918	17	CAA11819	3668118	hypothetical protein [Brassica napus]
---	912	19	CAB38785	4490294	WD-repeat protein-like protein [Arabidopsis thaliana]
---	912	19	AAF14048	6491862	putative cdc20 protein [Arabidopsis thaliana]
---	902	19	CAB38784	4490293	WD-repeat protein-like protein [Arabidopsis thaliana]
---	901	3	AAL28117	16755857	CDC20-like 1b [Homo sapiens]
---	900	3	BAA86955	6463685	Fzr2 [Homo sapiens]
---	892	19	NP_198109	15240985	fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
---	885	3	EAA05793	21293648	agCP10238 [Anopheles gambiae str. PEST]
---	882	3	AAC06232	2981095	Cdc20 [Spisula solidissima]
---	878	3	AAA83150	1109772	Method: conceptual translation suppl: 1 [Anopheles gambiae str. PEST]
---	868	19	NP_198060	15240441	fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
---	868	19	AAD48933	5732032	contains similarity to Pfam family P1 [Arabidopsis thaliana]
---	867	19	AAB61049	2191163	contains similarity to beta transducin-like modulator [Arabidopsis thaliana]
---	867	19	NP_198042	15240403	fizzy-related (FZR), putative; protein id: At5g13840.1 [Arabidopsis thaliana]
---	866	3	AAC41376	3298595	fizzy1 [Xenopus laevis]
---	863	3	AAC14741	3088632	cell cycle protein p55CDC [Rattus norvegicus]
---	861	3	AAH03215	13096838	Similar to cell cycle protein p55CDC [Arabidopsis thaliana]
---	860	3	AAA19017	468032	p55CDC [Homo sapiens]

860	3	AAH00624	12653679	CDC20 (cell division cycle 20, S. ce
860	3	BAA97451	8885513	Cdc20 [Mus musculus]
860	3	AAD16405	4323528	cell cycle protein CDC20 [Homo sapien
859	3	AAA19018	468034	p55CDC [Rattus norvegicus]
854	3	BAB27422	12847059	cell division cycle 20 homolog (S. ce
850	13	AAB63030	2253631	WD-repeat protein [Daucus carota]
833	3	CAA96703	1322451	ORF YGL003c [Saccharomyces cerevisiae]
793	3	AAC49621	1794292	WD-domain protein [Schizosaccharomyces
758	19	NP_568505	18421178	fizzy-related (FZR), putative; protei
744	3	CAB98424	15426166	probable hypothetical 13.7 Kd protein
692	3	AAK29632	13549094	p55CDC [Sus scrofa]
689	3	AAD26623	4633085	fizzy-related protein [Homo sapiens]
661	3	P26309	461700	Cell division control protein 20
661	3	BAA03957	416288	ORF1 [Saccharomyces cerevisiae]
632	3	CAD25313	19068845	CDC20-LIKE PROTEIN [Encephalitozoon c
573	3	BAC04508	21754461	unnamed protein product [Homo sapiens]
565	3	AAL31948	16930525	CDH1-B [Gallus gallus]
560	3	CAA42058	3645	Cdc20 [Saccharomyces cerevisiae]
517	3	AAB51112	1915987	CDC20 [Tritrichomonas foetus]
484	3	CAD26295	19168776	similarity to CDC20 (WD-repeat protei
457	3	XP_138861	20898546	similar to fizzy1 [Mus musculus]
400	3	CAA91101	1008993	putative cdc protein; WD repeat [Schiz
393	3	NP_011741	6681847	Required for sporulation, highly induc
392	3	AAK61800	14486175	Amalp [Saccharomyces cerevisiae]
389	3	CAA22488	4008571	putative WD-domain protein [Schizosac
358	3	XP_139652	20896939	similar to cell division cycle 20 homolog
350	3	AAL31950	16930529	CDH1-D [Gallus gallus]
333	3	AAG00051	9803044	Hypothetical protein ZK177.6 [Caenorh
287	3	T27762	7511009	hypothetical protein ZK177.6 - Caenorh
284	3	CAD01127	16416039	related to fzs protein [Neurospora crassa]
281	3	XP_142169	20985567	similar to cell cycle protein p55CDC
277	2	BAB75165	17132599	WD-40 repeat protein [Nostoc sp. PCC
257	2	BAB76258	17133695	WD-40 repeat-protein [Nostoc sp. PCC
248	2	BAB72396	17129783	serine/threonine kinase with WD-40 re
248	3	BAB97393	21322756	G6VTS76519 minor form-1 [Homo sapiens]
248	3	XP_094210	22050291	similar to G6VTS76519 minor form-1 [Homo sapiens]
247	3	AAK29631	13549092	fizzy-related protein FZR [Sus scrofa]
244	2	BAB74499	17131893	WD-repeat protein [Nostoc sp. PCC 71%
291	2	BAB77807	17135261	WD-40 repeat protein [Nostoc sp. PCC 71%
226	2	BAB78213	17135667	WD-repeat protein [Nostoc sp. PCC 71%
224	3	AAD35017	4973280	Ebi [Drosophila melanogaster]
247	2	BAB77771	17135225	WD-40 repeat protein [Nostoc sp. PCC 71%
223	2	BAB76458	17133896	WD-repeat protein [Nostoc sp. PCC 71%
222	3	AAB81475	9931971	general transcriptional repressor Tup1
222	3	CAB52736	5734475	general transcriptional repressor tup1
219	3	CAC81004	18076173	transcriptional repressor, TUP1 [Yarrowia
252	2	BAB74818	17132214	ORF_ID:alr3119-WD repeat protein with
210	2	BAC08041	22294210	WD-40 repeat protein [Thermosynechococcus
207	2	AAM05961	19916545	WD-domain containing protein [Methanococcus
222	3	AAL37301	17225210	beta transducin-like protein HET-D2Y
202	3	AAC29438	3406654	transcriptional repressor TUP1 [Dictyostelium
202	3	AAG28504	11066216	TUPA [Emericella nidulans]
212	2	BAB72622	17130010	WD-40 repeat protein [Nostoc sp. PCC 71%
201	3	T49342	11289987	fzs related protein [imported] - Neurospora
200	3	AAK93119	15291701	LD24014p [Drosophila melanogaster]
200	3	AAF51974	7296695	CG1109 gene product [Drosophila melanogaster]
237	2	BAB77808	17135262	WD-40 repeat protein [Nostoc sp. PCC 71%
197	3	AAB37245	1698504	rco-1 gene product [Neurospora crassa]
197	3	Q17963	3123159	HYPOTHETICAL 40.4 KD TRP-ASP REPEATS
195	3	AAH01353	12655011	katulin p80 (WD40-containing) subunit
195	3	BAB26884	12845754	data source:SPTR, source key:060620,
195	3	XP_134311	20885985	katulin p80 (WD40-containing) subunit



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J1: DNA Res 1997 Jun 30;4(3):215-30

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Structural analysis of *Arabidopsis thaliana* chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones.

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Sato S, Kotani H, Nakamura Y, Kaneko T, Asamizu E, Fukami M, Miyajima N, Tabata S.

Kazusa DNA Research Institute, Chiba, Japan.

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A total of 20 P1 clones with an average insert size of 80 kb and each containing a marker(s) specifically mapped on chromosome 5 were isolated from a P1 library of the *Arabidopsis thaliana* genome, and their nucleotide sequences were determined according to a shotgun-based strategy and precisely located on the physical map of chromosome 5 separately constructed. The total length of the sequenced regions were summed up to 1,621,245 bp. By comparison with the sequences in protein and EST databases and analysis with computer programs for gene modeling, a total of 347 potential protein-coding genes and/or gene segments with known or predicted functions were identified. The positions of exons which do not exhibit any similarity to known genes were also predicted. An average density of the genes and/or gene segments assigned so far as 1 gene/4,672 bp. Introns were identified in approximately 78% of the potential genes, and the average number and length of the introns per gene were 3.7 and 161 bp. The transcription level of the predicted genes was roughly monitored by counting the numbers of identified *Arabidopsis* ESTs. The sequence data and gene information are available through the World Wide Web at <http://www.kazusa.or.jp/arabi/>.

MeSH Terms:

- *Arabidopsis/genetics**
- *Chromosome Mapping**
- *DNA, Plant/analysis**
- *Genetic Markers/genetics*
- *Genomic Library**
- *Open Reading Frames**
- *Sequence Analysis, DNA*
- *Support, Non-U.S. Gov't*

Substances:

- *Genetic Markers*

- DNA, Plant

Secondary source id:

- GENBANK/AB005249
- GENBANK/AB005248
- GENBANK/AB005247
- GENBANK/AB005246
- GENBANK/AB005245
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- GENBANK/AB005230

PMID: 9330910 [PubMed - indexed for MEDLINE]

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